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Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
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Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
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Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys
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Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
100 105 110

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Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
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Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
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Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
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Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu
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Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser
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Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys
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25

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Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile
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Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala
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ccccaccaga tcggtaccat tgtaaatgcc aagaaagatg ttgtgaacac aaagatgttt 540
gaggagctca agagccgtct ggacaccctg gcccaggagg tggccctgct gaaggagcag 600
caggccctgc agacggtctc cctgaagggt ctagaacaaa aactcatctc agaagaggat 660
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<211> 711

<212> DNA

<213> Artificial

<220>

<223> AD1D4-GSS-I10-tripB

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cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaatg ctgcggggc 120
caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac 180
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt 240
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aggccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgccggctg 360
cgcaagtgcc gccccggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 420
tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttcagg 480
ccccaccaga tcggtaccat tgtaaatgcc aagaaagatg ttgtgaacac aaagatgttt 540
gaggagctca agagccgtct ggacaccctg gcccaggagg tggccctgct gaaggagcag 600

caggccctgc agacggtctc cctgaagggt ctagaacaaa aactcatctc agaagaggat	660
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caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac	180
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt	240
agctctgacc aggtggaaac tcaaggcctgc actcggaac agaaccgcat ctgcacctgc	300
aggccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgccggcgtg	360
cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg	420
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cccccaccaga tctgtAACGT ggtggccatc cctggaaatg caagcatgga tgcagtctgc	540
acgtccacgt ccccccacccg gagtatggcc ccagggcag tacacttacc ccagccagtg	600
tccacacgat cccaaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc	660
ttcctgctcc caatgggccc cagcccccca gctgaaggga gcactggcga cggtaccatt	720
gttaaatgcca agaaagatgt tgtgaacaca aagatgttt aggagctcaa gagccgtctg	780
gacaccctgg cccaggaggt ggcctgctg aaggagcagc aggccctgca gacggtctcc	840
ctgaagggtc tagaacaaaa actcatctca gaagaggatc tgaatagcgc cgtcgaccat	900
catcatcatc atcattgaaa gctgaattcc	930
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caacatgcaa aagtcttctg taccaagacc tcggacacccg tgtgtgactc ctgtgaggac	180
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt	240
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aggccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgccggcgtg	360
cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg	420
tgcagaaggcct gtccccggg gacgttctcc aacacgactt catccacgga tatttgcagg	480
ccccaccaga tctgtAACGT ggtggccatc cctggaaatg caagcatgga tgcagtctgc	540
acgtccacgt cctccgggtc ctccggtaacc gttgtgaaca caaagatgtt tgaggagctc	600
aagagccgtc tggacaccct ggcccaggag gtggccctgc tgaaggagca gcaggccctg	660
cagacgggtct ccctgaaggg tctagaacaa aaactcatct cagaagagga tctgaatagc	720
gccgtcgacc atcatcatca tcatcattga aagctgaatt cc	762
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caacatgcaa aagtcttctg taccaagacc tcggacacccg tgtgtgactc ctgtgaggac	180
agcacataca cccagctctg gaactgggtt cccgagtgct tgagctgtgg ctcccgctgt	240
agctctgacc aggtggaaac tcaagcctgc actcggaac agaaccgcat ctgcacctgc	300
aggccggct ggtactgcgc gctgagcaag caggaggggt gccggctgtg cgccggctg	360
cgcaagtgcc gcccgggctt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg	420
tgcagaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tattgcagg	480
ccccaccaga tctgtaacgt ggtggccatc cctggaaatg caagcatgga tgcagtctgc	540
acgtccacgt cccccacccg gagtatggcc ccagggcag tacacttacc ccagccagt	600
tccacacgat cccaaacacac gcagccaact ccagaaccca gcactgctcc aagcacctcc	660
ttcctgctcc caatggggcc cagccccca gctgaaggga gcactggcga cggtaaccgtt	720
gtgaacacaa agatgtttga ggagctcaag agccgtctgg acaccctggc ccaggaggtg	780
gccctgctga aggagcagca ggcctgcag acggctccc tgaagggtct agaacaaaaa	840
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<210> 96
 <211> 181
 <212> PRT
 <213> Homo sapiens

<400> 96

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp			
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Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr			
20	25	30	

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr			
35	40	45	

Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe			
50	55	60	

Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
65 70 75 80

Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
85 90 95

Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
100 105 110

Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val Asp Met Thr Gly
115 120 125

Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
130 135 140

Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
145 150 160

Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
165 170 175

Gln Phe Gly Ile Val
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<210> 97
<211> 137
<212> PRT
<213> Homo sapiens

<400> 97

Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys
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Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp
20 25 30

Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu
35 40 45

Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala
50 55 60

Glu Ile Trp Leu Gly Leu Asn Asp Met Ala Ala Glu Gly Thr Trp Val

65

70

75

80

Asp Met Thr Gly Ala Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile
85 90 95

Thr Ala Gln Pro Asp Gly Gly Lys Thr Glu Asn Cys Ala Val Leu Ser
100 105 110

Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu
115 120 125

Pro Tyr Ile Cys Gln Phe Gly Ile Val
130 135

<210> 98
<211> 102
<212> DNA
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<220>
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<210> 99
<211> 94
<212> DNA
<213> Artificial

<220>
<223> TN-lib2-tprev

<220>
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<222> (17)..(17)
<223> randomised

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<222> (18)..(18)
<223> randomised

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<400> 99

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cgccatacaag aactggaga ctgagatcac cgcg	94
<210> 100	
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csnnnsnnnn snnsnnnnna tcgggttgcg cggatctc agtctccc	108
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<212> DNA	
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<223> randomised

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<222> (72)..(73)
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csnnnsnnn snnatcgggt tgcgcggtga tctcagtctc cc                         102

<210> 102
<211> 137
<212> PRT
<213> Artificial

<220>
<223> TN3-2

<400> 102

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Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp
20          25            30

Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu
35          40            45

Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala
50          55            60

Glu Ile Trp Leu Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Met
65          70            75          80

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Asp Met Thr Gly Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile
85 90 95

Thr Ala Gln Pro Asp Pro Arg His Thr Glu Asn Cys Ala Val Leu Ser
100 105 110

Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu
115 120 125

Pro Tyr Ile Cys Gln Phe Gly Ile Val
130 135

<210> 103
<211> 137
<212> PRT
<213> Artificial

<220>
<223> TN3-2-B

<400> 103

Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys
1 5 10 15

Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp
20 25 30

Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu
35 40 45

Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala
50 55 60

Glu Ile Trp Leu Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Met
65 70 75 80

Asp Met Thr Gly Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile
85 90 95

Thr Ala Gln Pro Asp Pro Thr Asn Asn Glu Asn Cys Ala Val Leu Ser
100 105 110

Gly Ala Ala Asn Gly Lys Trp Phe Gly Lys Arg Cys Arg Asp Gln Leu
115 120 125

Pro Tyr Ile Cys Gln Phe Gly Ile Val
130 135

<210> 104
<211> 137
<212> PRT
<213> Artificial

<220>
<223> TN3-2-C

<400> 104

Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys
1 5 10 15

Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp
20 25 30

Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu
35 40 45

Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala
50 55 60

Glu Ile Trp Leu Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Val
65 70 75 80

Asp Met Thr Gly Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile
85 90 95

Thr Ala Gln Pro Asp Pro Thr Asn Arg Glu Asn Cys Ala Val Leu Ser
100 105 110

Gly Ala Ala Asn Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu
115 120 125

Pro Tyr Ile Cys Gln Phe Gly Ile Val
130 135

<210> 105
<211> 137
<212> PRT
<213> Artificial

<220>

<223> TN3-2-D

<400> 105

Ala Leu Gln Thr Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys
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Phe Leu Ala Phe Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp
20 25 30

Cys Ile Ser Arg Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu
35 40 45

Asn Asp Ala Leu Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala
50 55 60

Glu Ile Trp Leu Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Ile
65 70 75 80

Asp Met Thr Gly Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile
85 90 95

Thr Ala Gln Pro Asp Pro Asn Asn Arg Glu Asn Cys Ala Val Leu Ser
100 105 110

Gly Ala Ala Asn Gly Lys Trp Phe Gly Lys Arg Cys Arg Asp Gln Leu
115 120 125

Pro Tyr Ile Cys Gln Phe Gly Ile Val
130 135

<210> 106

<211> 181

<212> PRT

<213> Artificial

<220>

<223> TN-2-B

<400> 106

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
1 5 10 15

Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
20 25 30

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
35 40 45

Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
50 55 60

Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
65 70 75 80

Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
85 90 95

Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
100 105 110

Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Met Asp Met Thr Gly
115 120 125

Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
130 135 140

Asp Pro Thr Asn Asn Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
145 150 155 160

Gly Lys Trp Phe Gly Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
165 170 175

Gln Phe Gly Ile Val
180

<210> 107
<211> 181
<212> PRT
<213> Artificial

<220>
<223> TN-2-D

<400> 107

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
1 5 10 15

Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr

20

25

30

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
35 40 45

Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
50 55 60

Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
65 70 75 80

Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
85 90 95

Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
100 105 110

Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Ile Asp Met Thr Gly
115 120 125

Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
130 135 140

Asp Pro Asn Asn Arg Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
145 150 155 160

Gly Lys Trp Phe Gly Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
165 170 175

Gln Phe Gly Ile Val
180

<210> 108

<211> 181

<212> PRT

<213> Artificial

<220>

<223> TN-2-C

<400> 108

Glu Pro Pro Thr Gln Lys Pro Lys Lys Ile Val Asn Ala Lys Lys Asp
1 5 10 15

Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys Ser Arg Leu Asp Thr
20 25 30

Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln Gln Ala Leu Gln Thr
35 40 45

Val Cys Leu Lys Gly Thr Lys Val His Met Lys Cys Phe Leu Ala Phe
50 55 60

Thr Gln Thr Lys Thr Phe His Glu Ala Ser Glu Asp Cys Ile Ser Arg
65 70 75 80

Gly Gly Thr Leu Ser Thr Pro Gln Thr Gly Ser Glu Asn Asp Ala Leu
85 90 95

Tyr Glu Tyr Leu Arg Gln Ser Val Gly Asn Glu Ala Glu Ile Trp Leu
100 105 110

Gly Leu Asn Lys Val Arg Ser Arg Tyr Phe Trp Val Asp Met Thr Gly
115 120 125

Thr Arg Ile Ala Tyr Lys Asn Trp Glu Thr Glu Ile Thr Ala Gln Pro
130 135 140

Asp Pro Thr Asn Arg Glu Asn Cys Ala Val Leu Ser Gly Ala Ala Asn
145 150 155 160

Gly Lys Trp Phe Asp Lys Arg Cys Arg Asp Gln Leu Pro Tyr Ile Cys
165 170 175

Gln Phe Gly Ile Val
180

<210> 109
<211> 256
<212> PRT
<213> Artificial

<220>
<223> AD1D4-GSS-I10

<400> 109

Met Gly Ser Met Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro
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Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met
20 25 30

Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr
35 40 45

Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr
50 55 60

Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys
65 70 75 80

Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg
85 90 95

Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu
100 105 110

Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly
115 120 125

Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys
130 135 140

Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg
145 150 155 160

Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser Met
165 170 175

Asp Ala Val Cys Thr Ser Thr Ser Ser Gly Ser Ser Gly Thr Ile Val
180 185 190

Asn Ala Lys Lys Asp Val Val Asn Thr Lys Met Phe Glu Glu Leu Lys
195 200 205

Ser Arg Leu Asp Thr Leu Ala Gln Glu Val Ala Leu Leu Lys Glu Gln
210 215 220

Gln Ala Leu Gln Thr Val Ser Leu Lys Gly Leu Glu Gln Lys Leu Ile
225 230 235 240

Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His His His
245 250 255